

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 22:53:44 ; Search time 33.32 Seconds
(without alignments)
2110.117 Million cell updates/sec

Title: US-09-497-822a-19
Perfect score: 4912
Sequence: 1 MEVGLGRVYPPPSKTYR.....SVQPKILSGKVKPIYFHTQ 923

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	ID	Description
1	4880	99.3	919	2 A39248	androgen receptor
2	4798.5	97.7	910	2 A34721	androgen receptor
3	4763	97.0	911	2 B34721	androgen receptor
4	4206.5	85.6	902	2 B40494	androgen receptor
5	4176	85.0	899	2 A35895	androgen receptor
6	1676	34.1	344	2 I51330	androgen receptor
7	1523	31.0	848	2 JG0194	androgen receptor
8	1262.5	25.7	930	2 A25923	progesterone recep
9	1262	25.7	933	1 QRHUP	progesterone recep
10	1234	25.1	923	2 I53280	progesterone recep
11	1218	24.8	786	2 A35466	progesterone recep
12	1205	24.5	923	2 A39596	progesterone recep
13	1092	22.2	981	2 A14101	mineralocorticoid
14	1078.5	22.0	984	2 A29513	glucocorticoid rec
15	1065	21.7	795	1 QRRTG	glucocorticoid rec
16	1063.5	21.7	783	1 A25691	glucocorticoid rec
17	1054.5	21.5	776	1 S44047	glucocorticoid rec
18	1042	21.2	777	1 QRHUGA	glucocorticoid rec
19	1023	20.8	758	2 S60586	glucocorticoid rec
20	1003	20.4	771	2 A54273	glucocorticoid rec
21	943.5	19.2	742	1 QRHUGB	glucocorticoid rec
22	715	14.6	166	2 S35795	estradiol receptor
23	502	10.2	595	2 I47140	estrogen receptor
24	491	10.0	586	1 ORXLE	estrogen receptor
25	485.5	9.9	600	1 ORSTE	estrogen receptor
26	478	9.7	595	1 QRHUE	80K estrogen recep
27	478	9.7	701	2 S64737	estrogen receptor
28	474	9.6	589	1 QRCH	
29	474	9.6	599	1 QRMSE	

30	461.5	9.4	620	2 T10423	estrogen receptor
31	448	9.1	535	2 S58224	estrogen receptor
32	444	9.0	574	2 A37197	estrogen receptor
33	442	9.0	503	2 JN0046	estrogen receptor
34	437.5	8.9	477	2 S71400	estrogen receptor
35	437.5	8.9	530	2 JG5939	estrogen receptor
36	398.5	8.1	1043	2 T13733	estrogen receptor
37	391	8.0	433	2 S58087	estrogen receptor
38	387.5	7.9	433	2 B29345	estrogen receptor
39	383	7.8	521	2 A29345	estrogen receptor
40	379	7.7	462	2 S44490	estrogen receptor
41	370.5	7.5	543	2 A32693	estrogen receptor
42	364.5	7.4	746	2 B32693	estrogen receptor
43	357	7.3	533	2 S37781	estrogen receptor
44	346	7.0	422	2 I48305	estrogen receptor
45	343.5	7.0	423	2 S02710	estrogen receptor

ALIGNMENTS

RESULT 1
A39248
androgen receptor - human
C:Species: Homo sapiens (man)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 24-Nov-1999
C:Accession: A39248; A30328; A60946; A34942; A27653; A40108; A40494; A32224;
R:Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgins, H.N.; Migeon, C.J.; Wilson, E.M.;
Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989
A:Title: Sequence of the intron/exon junctions of the coding region of the human andr
A:Reference number: A39248; MUID:90083302
A:Accession: A39248
A:Molecule type: DNA
A:Residues: 1-919 <LUB>
A:Cross-references: GB:M27423; GB:M27430; NID:gl78904; PIDN:AAA51886.1; PID:gl78906
R:Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Brinkma
Mol. Cell. Endocrinol. 61, 257-262, 1989
A:Title: The N-terminal domain of the human androgen receptor is encoded by one, larg
A:Reference number: A30328; MUID:89137730
A:Accession: A30328
A:Molecule type: DNA
A:Residues: 1-77,79-165, 'A', 167-389, 'L', 391-464, 473-538 <FAB>
A:Cross-references: GB:M20260
R:Lubahn, D.B.; Joseph, D.R.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, F.
Science 240, 327-330, 1988
A:Title: Cloning of human androgen receptor complementary DNA and localization to the
A:Reference number: A40109; MUID:88178112
A:Accession: A40109
A:Molecule type: DNA
A:Residues: 559-624 <LUB>
A:Cross-references: GB:M20132
R:Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Ris-Sta
J. Mol. Endocrinol. 2, 1265-1275, 1988
A:Title: Structural organization of the human androgen receptor gene.
A:Reference number: A60946; MUID:89322749
A:Accession: A60946
A:Molecule type: DNA
A:Residues: 536-540; 587-591; 626-631; 723-726; 770-774; 814-818; 867-870 <KUI>
R:Lubahn, D.B.; Joseph, D.R.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, F.
Mol. Endocrinol. 2, 1265-1275, 1988
A:Title: The human androgen receptor, complementary deoxyribonucleic acid cloning, se
A:Reference number: A34942; MUID:89112208
A:Accession: A34942
A:Molecule type: mRNA
A:Residues: 1-919 <LUB>
A:Cross-references: GB:M20132; NID:gl78627; PIDN:AAA51729.1; PID:gl78628; GB:J03180
R:Trapani, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Faber, P.W.;
Biochem. Biophys. Res. Commun. 153, 241-248, 1988
A:Title: Cloning, structure and expression of a cDNA encoding the human androgen rece
A:Reference number: A27653; MUID:88240407
A:Accession: A27653
A:Molecule type: mRNA
A:Residues: 468-564, 'K', 566-919 <TRA>

[illegible]

[illegible]

Query Match	25.7%	Score 1262.5;	DB 2;	Length 930;
Best Local Similarity	33.8%;	Pred. No. 2e-59;		
Matches 336; Conservative 122;	Mismatches 308;	Indels 227;	Gaps 31;	
QY	1	MEVQLGLGRVTPRPSTKTYRGAFNQFSVREVIQNPF-----G	38	
		: : : :		
Ddb	91	VZAPGAGDSSRRPEKD-----SGLLDSDLTLAPSGPGQSHASPATCEAISPWCLF	145	
QY	39	PRHPEAAZAAPPASLLLLLQQQQQQQQQQQQQQQQQQQQQTSPRQQQQQGGDS	98	
		: : : :		
Ddb	146	POLPEDPRAAAPATKGVL-----APLMSPEDKAGDSGT	179	
QY	99	PQAHR---RG--PTGYLVILDEEQPQSOPSALECHPERGCVPPEGAAVAASKGLPOOLPA	153	

459 GGGGGGGGGGGGGGGAAGAVPYGTRPPGOLAGQESDFTAPDVWPGMVSR-VPY 517
 486 SGCLLPDGLPSTASAAAAGA-APALY--PALGLNG-----LPQLGYOAAVLKESGLPQ 536
 518 PSPTCVKSEKMPWMDSYSGPYGDMRLTARDHVLPIIDYPP--PQKTLICGDEASGCHY 575
 537 VYPPYL-NYLRPDSEASQSP-----QYSEFSLPQKTLICGDEASGCHY 579
 576 GALTGCGCKVFFKRAAGKOKYLICASRNDCTIDKFERKNCPSRLRKCYEAGMTLGARKL 635
 580 GVLTCGCKVFFKRAAGKOKYLICASRNDCTIDKIRKNCPCALRKCCOAGNVLGKRF 639
 636 KKLGNLKLQEEGEASSTSP-----TEETQKLTIVSHIEGYEQPIFLNVLEAIEPVV 689
 640 KFKNVVRVRAIDVALPOLPLGVNPSOALSQRFTSPGQDQIOLPLILNLLMSIEPDVI 699
 690 CAGHNDNQPSFAALLSSELGERQLVHVWVWAKALPGFRNLHVDDQMAVIOYSWGLM 749
 700 YAGHNDTKPDTSLSLTLNOLGERQLVHVWVWAKALPGFRNLHVDDQMAVIOYSWGLM 759
 750 VFAMGWSFTVNSRMVLYFADIVFENYHMKSRMYSQCVMRHLSQEFGLWLTTPQEF 809
 760 VEGWGRSYKIVSQMQLYFADILNENQMKESFYSLCTMQLPQEFVQLQVSOEFL 819
 810 CMKALLFSIIPVGLKNQKFFDELWNYIKELDRITACKRNKPTSCRRFYQLTKLDS 869
 820 CMKVLNLTNPTEGLRSQTOFEEMRSYIRELIKATIGLQKGVVSSORFYQLTKLDS 879
 870 VOPIARELHQFTDLLIKSHMVVDPEMMAEILISVQVPKILSGKVPYVFH 921
 880 LHDVLQHLHLCLNTFFIQSRALSVEFPEMSEVIAAQLPKILAGWVPLLFH 931

RESULT 10
 153280
 progesterone receptor B form - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_1996 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: U53280; U53280; A49574; A23733
 R:Park, O.K.; Mayo, K.E.
 Endocrinology 134, 709-718, 1994
 A:Title: Regulation of the progesterone receptor gene by gonadotropins and cyclic adenosine
 A:Reference number: U53280; MUID:94130817
 A:Accession: U53280
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-923 <PAR1>
 A:Cross-references: GB:L16922; NID:g463282; PIDN:AAA19916.1; PID:g463283
 R:Park, O.K.; Mayo, K.E.
 Mol. Endocrinol. 5, 967-978, 1991
 A:Title: Transient expression of progesterone receptor messenger RNA in ovarian granulosa
 A:Reference number: A23733; MUID:92049379
 A:Accession: U53280
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 555-589, 'W', 591-624, 742-910 <PAR2>
 A:Cross-references: GB:S64044
 R:Kraus, W.L.; Montano, M.M.; Katzenellenbogen, B.S.
 Mol. Endocrinol. 7, 1603-1616, 1993
 A:Title: Cloning of the rat progesterone receptor gene 5'-region and identification of the
 A:Reference number: A49574; MUID:94195318
 A:Accession: A49574
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <KRA>
 A:Cross-references: GB:S69361; NID:g546178
 C:Superfamily: progesterone receptor; erba transforming protein homology
 C:Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
 F:555-819/Domain; erba transforming protein homology <ERBA>
 F:557-577/Region; zinc finger
 F:593-617/Region; zinc finger

Query Match 25.1%; Score 1234; DB 2; Length 923;
 Best Local Similarity 33.1%; Pred. No. 6.3e-56;
 Matches 344; Conservative 129; Mismatches 299; Indels 266; Gaps 39;

QY 15 PSKTYRGA-----FQNLFSQSVREVIONPGPRHPEAASAAAPP-----GASLLLLLOQQQ 61
 DB 19 PSPTWVGSPLARLDPPFQ-----GSHSDASSVVSPIFSLDRLLFSRSC 65
 QY 62 QQQQQQQQQQQQQQQQ-----QQQQQQQETSPROQQQQQGGEDGSPQARRGPTGYL 110
 DB 66 QQAQLPDEKTONQOQSILSDVEGAFCGVEASRRRRRNPRAPKEDSRLLDS----- 113
 QY 111 VLDEFOQPSOPSALECHPERG-----VPEPGAAVAASKGLPOOLPAPPDE- 157
 DB 114 VLDITLAPSGPEQSOTSPP--ACEAITSWCLFPGPELDPDRSVKATKLLSPLMSRPSK 171
 QY 158 --DSSAA-----PSTLS-----LLGPTF-----PGLSSCSADLKD---ILSEA 190
 DB 172 AGDSSGTGAGOKVLPKAVSPPRQLLPTSGSAHWPGAGVKPSQQPATVEVEDGGLTEG 231
 QY 191 STMQLLQQQQQEAIVSEGSSGGRARASGAPTSSKDNYLGGTSTI--SDNAKELCKAVSYM 249
 DB 232 SAGPLLKSKPRALEGCMCGGGVTANAPGAAP-----GGVTLVPKEDSRFSAPRVSLQ 284
 QY 250 GLGV-----EALHLSPEQQLRGDCM-----YAPLLGV 277
 DB 285 DAPVAPGRSPLATTVVDFTHVPLPLNHALLAARTQLLEGDSYDGGAAAVQVFPAPRGS 344
 QY 278 PPAVR--PTPCAPLAECKGLLDDSGAKSTED--TAEYSPKPGYTKGLGESLCSGSA 335
 DB 345 PSAPSPVPVPCGDFPDC-----TYPPEGDPKEDGFVYGEFQPPGLKIKEE-----EGTEAA 396
 QY 336 GSSGTELEPSTLSLYKSGALDEAAVQSRDYNFPLALAGPPPPP--PPHPHARIKLEN 393
 DB 397 SRS-----PRPYLL-----AGASAAATFPDFPL-----PPRPPAPSRP----- 430
 QY 394 PLDYGSAWAAAAQCRYGDIAS-----LHGAGAAGPGSGS-----PSAAASSSWH 438
 DB 431 ---GEA-AVAAPSAAVSPVSSSGSALECYLKAEGAPPTGSGFAPLPCKPPAAS- 481
 QY 439 TLFTAEGQLYPCGCGGG 498
 DB 482 -CULPRDLSAAP-----TSSAAPAIY--PLGLNG--- 509
 QY 499 DFTAPDVWYPCGMV-SRVVPYSPCTCVKSEMPMD-----SYSGPYGDMRLTARDH 549
 DB 510 --LPQLGYOAAVLKDSLPQVY-----PYLNLVRPDSASQSPQYCFDSL----- 552
 QY 550 VLPTDYFPQKTLICGDEASCHYCALTCGSKVFFKRAAGKOKYLICASRNDCTIDK 609
 DB 553 -----PQKTLICGDEASCHYGVLTGCGSKVFFKRAAGKOKYLICASRNDCTIDK 603
 QY 610 FRKNCPSRLRKCYEAGMTLGARKLKLGNLQLE--EGEA--SSTTSPTEFT--QKL 663
 DB 604 IRRKNCPCALRKCCOAGVGLGKFKFNKVRMRALDQVALPQSVAFPNESQITGQRI 663
 QY 664 TVSHIEGYEQPIFLNVLEAIEPGVVCAGHNDNQPSFAALLSSELGERQLVHVWVW 723
 DB 664 TFSNQETQLVPLPLINLMSIEPDVYVAGHDNTKPDTSLSLTLNOLGERQLVHVWVW 723
 QY 724 KALPGFRNLHVDDQMAVIOYSWGLMVAFMGWRSFTVNSRMVLYFADIVFENYHMKSR 783
 DB 724 KSLPGFRNLHVDDQMAVIOYSWGLMVAFMGWRSFTVNSRMVLYFADIVFENYHMKSR 783
 QY 784 MYSOCVVRMRLHSQEFGLWLTTPQEFCKMALLFSIIPVGLKNQKFFDELWNYIKEL 843
 DB 784 FYSCLTWMQIPQEFVKLQVTHEFCKMALLFSIIPVGLKNQKFFDELWNYIKEL 843
 QY 844 RIACKRNKPTSCRRFYQLTKLDSVQPIARELHQFTDLLIKSHMVVDPEMMAEII 903
 DB 844 KAIGLRQKGVVPSORFYQLTKLDSLHDLVQLHKLQHLCLNTFFIQSRALAVEFPEMSEVI 903

Db 713 QKGVVANSQRYQLTKLMDSMHDLVKQLHLFLCLNTFLQSRALSVEFFEMMSEVIAAQLPK 772
Qy 910 ILSGKVPPIYFH 921
Db 773 ILAGWVAPLLFH 784
RESULT 12
A39596
Progesterone receptor B form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 20-Aug-1999
C:Accession: A39596; I49111
R:Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.
Biochemistry 30, 7014-7020, 1991
A:Title: Molecular cloning, sequence analyses, and expression of complementary DNA encoding the human progesterone receptor B form
A:Reference number: A39596; MUID:91299759
A:Accession: A39596
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-923 <SCH>
A:Cross-references: GB:M68915; GB:J05333; NID:g200471; PIDN:AAA39971.1; PID:g200472
R:Ragihara, K.; Wu-Peng X.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.
Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994
A:Title: Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the mouse progesterone receptor B form
A:Reference number: I49111; MUID:95100931
A:Accession: I49111
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <HAG>
A:Cross-references: EMBL:U12644; NID:9639916; PIDN:AAA66067.1; PID:g639917
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zinc finger
F:555-819/Domain: erba transforming protein homology <ERBA>
F:557-577/Region: zinc finger
F:593-617/Region: zinc finger

Query Match 24.5%; Score 1205; DB 2; Length 923;
Best Local Similarity 32.2%; Pred. No. 2.1e-56;
Matches 337; Conservative 119; Mismatches 301; Indels 288; Gaps 36;

Qy 35 QNPGPRHPAAASAAPP--GASILLQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQTSP----- 86
Db 7 KDPVLHTSGAFSPPHICGSPLL-----ARLDGPFQGSQSHSDVSVVPIPISLD 57
Qy 87 -----RQOQQQGGEDGSPQA-----HRRGPTYG-----IULD 113
Db 58 GLLFPRSCRGPELPDGKTGDQSLSDVEGAFSGVEATHREGGRNRPPEKDSRLDLSVD 117
Qy 114 EEOQPSQPSQSALECHPERGCVPEPGNAVAASKGLPQQLPAPPDDEDSAPSTLSLGTTF 173
Db 118 SLTTPSGPE---QSHAS-----PPACFAITISWCLFGPELP-----EDPRVPATKGLLSP-- 164
Qy 174 PGLSSCSADLKDTLSASTMQLLQOQQQPAVSESSGSRAREASCAPTSSKDNVLLGGTST 233
Db 165 -----LMSRPEIKVGDSQGTGRGQ----- 183
Qy 234 ISDNAKELKAVSVSMGLGVEALEHLSPEQL---RGDCMYAPLLGVPAVPTPCAPLA 290
Db 184 -----KVLPGK-----LSPPRQLLPTSGSAHPGAGVKPS--PQPA----- 219
Qy 291 ECKGSLDLSAGKSTEDTAESYFPGKGGYTKLGESLG---CSGSAAGSGSTLELPSTL 347
Db 220 ---GEVEEDS-GLETEGSA--SPLLKSKPRALEGTGQGGVGAANAPSAAPGGVTLVPKED 273
Qy 348 SLXKSGALD-----EAAAYQSRDYNNPL-----A 372
Db 274 SRSAPRVSLQSDSPIAPGKSLPATTWDFIHWPIPLNHALLAARTROLLEGESYDGA 333
Qy 373 LAGPFPFPFPFP-----HPHAKIKLEN-----PLDYGSAWAAAAACRYGDLA 414

Db 334 TAGPCPCPRSPSAPSTPVPRGDFPDCTYPLEGDKPEDVEPL-----YGDQ 379
Qy 415 S-----LHGAGAAGPGSGSP-----SAAASSWHITLFTAEAGQLYPCPCGGGGGGGG 462
Db 380 TPGLKIKBEEEGADAA---VRSRPRYLSAGASSSTFPDFPLAPAPQAAPSSRSGEAAVAG 436
Qy 463 GGGGGGGGGGGGGA-----GAVAPYGVTRPP-----QGLAGQESD 499
Db 437 GPSSAAVSPASSGSALECILYKAEAPTQGSFAPLP-CKPAAASCLLPRDPLPAAPGT 495
Qy 500 FTAPDVMYFPGMVSRVPYPTCVKSEMPMDSYSGYGDMMRLTARDHVLPL--IDYFF 557
Db 496 AAPAIYQPLGL-NGPL-----YQAAVLKDSLPPQYPPYLYNLRL 536
Qy 558 P-----POKTLICGDEASGCHYGALTGCSCKVFFKRAAEGKOKYLCASR 602
Db 537 PDSEASQSPQYGFDSLQPKICICIGDEASGCHYGVLTCGCKVFFKRAEGOHNYLCAGR 596
Qy 603 NDCITDKFRKNCPCRLRKYCAAGMTLGARKLKLGNLKLQE--EGEA--SSTTSPTTE 658
Db 597 NDCIVDKIRKNCPCACRLRKCQAGWVLGGRKFKFNKVRVMRTLGDVALPOSVGLPNE 656
Qy 659 --TTQKLTVSHIEGTECQDIFLNLEAIEPVGVCAGHDNNQPDFAALLSSNLGERQL 716
Db 657 QALSQRITFSPNQEIQLVPLPINLLMSIEPDVIYAGHDNTRKPDTSLSLTSUNQGERQL 716
Qy 717 VHVVKAKALPGFRNLHVDQNAVIOYSWMLVMTAMGRSFTNVNSRMLYFAPDLVNE 776
Db 717 LSVVKNWSKSLPGFRNLHIDDQITLQYSWMSLMVFLGWRSYKHVSGQMLYFAPDLILNE 776
Qy 777 YRMHKSRYSOCVVRMHLHQEFGLWQITPOEFLCMKALLFSIIPVDGLKNQKFFDELRLM 836
Db 777 QRMKELSFYSLCTLMQIPEQFVKLQVTHEEFLCMKVLLLNTIPLGLRSQSQFEEMRS 836
Qy 837 NYIKELDRIITACRKNPTSCSRREYOLTKLDSVQPIARELHOFTDILIKHMYSDVDP 896
Db 837 SYIRELKAIGLRKQGVVPTSQRFYOLTKLDSLHDLVKQLHLCLNTTIQSKTLAVEFP 896
Qy 897 EMMAETISVQVPRKILSGKVKPIYFH 921
Db 897 EMNSEVIAAQLPKILAGWVKPLLFH 921
RESULT 13
A14101
mineralocorticoid receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 20-Sep-1999
C:Accession: A14101
R:Patel, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.
Mol. Endocrinol. 3, 1877-1885, 1989
A:Title: Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA
A:Reference number: A14101; MUID:90114194
A:Accession: A14101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <PAT>
A:Cross-references: GB:M36074; NID:g205340; PIDN:AAA1583.1; PID:g205341
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:602-877/Domain: erba transforming protein homology <ERBA>
F:604-624/Region: zinc finger
F:640-664/Region: zinc finger

Query Match 22.2%; Score 1092; DB 2; Length 981;
Best Local Similarity 32.0%; Pred. No. 2.1e-50;
Matches 310; Conservative 119; Mismatches 306; Indels 234; Gaps 34;

Qy 77 QOQQOQQTSPR---QOQQOQGGEDGSPQAHRRGPTGYLVLDDEEQPSQPSA----- 124
Db 121 QOQQOQGSLSPTKIYQNMEQLVKFYKENGHRSSSTLS--AMSRPLRSFMPDASAASNGGALR 178

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125 -----LECHPERGCVPEP---GAAVAASKGL-----PQQLPAPDEDDNSA 162
Db 179 AIVKSPIICHEKSSSVSPLNMASSVCGPVGINSMSSTTSFGSPVHPSPITQGTSLTCS 238
Qy 163 PST-----LSLLGPTFPGLSSCADKDLSEASTMQLLOQ 198
Db 239 PSVENRGRSHSPHASNVGSPSSPLSSMKSPISPPSHCS--VKSPVSSPNVPLRSS 296
Qy 199 QOQEA-----VSEGGSGRAREASGAPTSKDNV LGCTSTISDNAKELCKAVSVSMG 250
Db 297 VSSPANLNNSRCSVSSPSNNTNRRSTLSSTASTVSGIG--SPISNATSYATSGASAG 354
Qy 251 LGVLEHLSPG-----EQLRGDCMYAPLLGVPPAVAPRTPCAPL-----ABCKGSLDD 299
Db 355 -----AIODVVPSPTDTEKGAHGVFPKTEVEKATNSGTGPNIVQYIKSEPDGAFSS 410
Qy 300 SAGKSTEDTAETSPKGGYTKLGESLGCSSAAAGSGTLELSTLSLYKSGALDEAA 359
Db 411 CLGNSK-ISPSPFFSVPTKQ---ESSKHSCSGASFKNPTNVPFPFMDGYSFS-FMDD-- 464
Qy 360 AYOSRDYNNPLALAGPPPP-----PPPPHPHARIKLENPLDYGSAAWAAAAQCRYGDL 413
Db 465 ---KDYLSLS-GILGPPVPGDSCEDSAFP---VGIKQEPDDGS-----YYPE 506
Qy 414 ASLHGAGAGPGSGSPSAASSWHTLFTAEEOQLYPCGGGGGGGGGGGGGGGGGG 473
Db 507 ASIPSSAIVGVNSG-----GQSFHY----- 526
Qy 474 GGGEAGAVAPYGYTRPPQGLAQESDFTAPDVWYPGMVSRVPYSPCTVKSEMGPNWDS 533
Db 527 ---RIGAQGTISLSRSPROGSFQH-----LSSFP-PVNTLVES-----WK-- 562
Qy 534 YSPGYGDMLETAARDHVLPIDYFP-----PQKTLICDEAGSCHYG 576
Db 563 ---PHGD--LSSRRSDGYPVLEYIPENVSSSTLSRVSTGSSRPSKICLVCGDEAGSCHYG 617
Qy 577 ALTGCGCKVFFKRAAGKOKYLCASRNDCTIDKFRKNCPCRLKCYEAGMTLGARKLK 636
Db 618 VVTGCGCKVFFKRAVEGQHNYICAGRNDCTIIDKIRKNCPCARLQKCLQAGMNLGARKSK 677
Qy 637 KIGNLK-LQEE-----GEASSTTSPTTEET-----QKLTYSHIGYECQP 675
Db 678 KLGLKLGLHEEQPQPPPPQSPPEGITYIAPTKEFSVNSALVPQLTSITH-----ALTP 733
Qy 676 IFNLVLEALEPGVVCAGHDNNQPSFAALLSSNELGERQLVHVVKWAKALPGFNLHVD 735
Db 734 SPAMILENIEPTVYAGYDNSKPDPTAESSLTLNRLAAKQMIQVVKWAKVLPFGFKNLPLE 793
Qy 736 DQMAVIOYSWMLGMVFMAGWRSFTNVNSRMLYFAPDLVFNEMRHKSMYSQCVRRHLS 795
Db 794 DQITLIOYSWMLSSSFALSWSRYSKHTNSQLLYFAPDLVFNEMRHKSMYSQCVRRHLS 853
Qy 796 OFEGWLOITPQBFLOWKALLFSIPVDGLKNKFFDELRMNYSIKELDRLIACKRNKPTS 855
Db 854 LQFVRLQUTFEYSIMVKVLLSTVPDGLKSQAFAEMRTNVIKELRMVNT---KCPNS 910
Qy 856 CS---RREYQTLTKLSDVPTARELHFTFDLLIKSHWSVDPEPMMAEIIISVQVFKILS 912
Db 911 SQSQWQRYEYQTLTKLSDMHDVLSLEFCFTTFRESQALKVPEFPAMLVEIITDQLPKVES 970
Qy 913 GKVKPIYFH 921
Db 971 GNAKPLYPH 979

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RESULT 14
A29513
mineralocorticoid receptor - human
N:Alternate names: aldosterone receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Sep-1999
C:Accession: A29513
R:Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, T.M.; Handelin, B.L.; Housman, D.E.

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Science 237, 268-275, 1987
A:Title: Cloning of human mineralocorticoid receptor complementary DNA: structural an
A:Reference number: A29513; MUID:87263386
A:Accession: A29513
A:Molecule type: mRNA
A:Residues: 1-984 <ARK>
A:Cross-references: GB:M16801; NID:g187460; PTDN:AAA59571.1; PID:g307166
C:Genetics:
A:Gene: GDB:MLR
A:Cross-references: GDB:120188; OMIM:264350
A:Map position: 4q31-4q31
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
F:601-880/domain: erba transforming protein homology <ERBA>
F:603-623/region: zinc finger
F:639-663/region: zinc finger

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Query Match 22.0%; Score 1078.5; DB 2; Length 984;
Best Local Similarity 32.8%; Pred. No. 1.1e-49;
Matches 300; Conservative 101; Mismatches 254; Indels 259; Gaps 30;

Qy 98 SPOAHRRGPTGYL-----VLDEEQP-SQPSALECHPERGCVPEP-----GAAVAASK 145
Db 238 SPNAENRGRSRSHPAHASNVGSPSSPLSSMKSSISSPSHCSVKSPVSSPNNTVLRSSV 297
Qy 146 GLPQQL-----PAPDEDD-----SAAPSTL-SLLGP-----TFPGLSSCSADLKD 185
Db 298 SSPANINNSRCSVSSPSNNTNRRSTLSSPAATVGSICSVPNNAFSYTASGTISAGSSTLRD 357
Qy 186 ILSEASTMQLLOQ---QOEA VSEGS SSGRA-----REASGAPTSSKDNLYLGGT 231
Db 358 VVPSPTDTEKGAQVFPKTEVEKATNSGTGPNIVQYIKPEPDGAFSS---CLGNN 414
Qy 232 STISDNAKELKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTCAPLAE 291
Db 415 SKINSDS-----SFSVPIKQESTKHCSCSTSPKGN-----PTVNPFP----- 451
Qy 292 CKGSLLDSDACKSTEDTAET---SPFKGGYTKLGESLGCSSAAAGSGTLELSTLSL 349
Db 452 ---FMDCSYF-SFMDKDYLSLGLGPPVPVPGDQ---NCEGS----- 487
Qy 350 YKSGALDEAAAAQSRDYNNFPLALAGPPPPPPPHPHARIKLENPLDYGSAAWAAAAQCR 409
Db 488 -----GFPVGIKQEP-----DDGS----- 501
Qy 410 YDGLASLHAGAGPGSGSPSAAAASSSWHTLFTAEEOQLYPCGGGGGGGGGGGGGGGG 469
Db 502 YYPEASIPSSAIVGVNSG-----GQSFHY----- 525
Qy 470 GGGGGGGEAGAVAPYGYTRPPQGLAQESDFTAPDVWYPGMVSRVPYSPCTVKSEMG 529
Db 526 -----RIGAQGTISLSRARDQSFOH-----LSSFP-PVNTLVES----- 559
Qy 530 WMDYSYCPGYGDMLETAARDHVLPIDYFP-----PQKTLICGDEASG 572
Db 560 WKS-----HGD--LSSRRSDGYPVLEYIPENVSSSTLSRVSTGSSRPSKICLVCGDEASG 612
Qy 573 CHYGALTCGCKVFFKRAAGKOKYLCASRNDCTIDKFRKNCPCRLKCYEAGMTLGA 632
Db 613 CHYGVTTCGCKVFFKRAVEGQHNYICAGRNDCTIIDKIRKNCPCARLQKCLQAGNNLGA 672
Qy 633 RKLKGLNLK-LQEEGEAS-----TTSPTTEET-----QKLTYSH 667
Db 673 RKSKKLGLKGLHEEQPQPPPPQSPPEGITYIAPAKEPSVNTALVPQLSTISR 732
Qy 668 IEGYECQPIFNLVLEALEPGVVCAGHDNNQPSFAALLSSNELGERQLVHVVKWAKALP 727
Db 733 ---ALTPSPVMVLENIEPTVYAGYDNSKPDPTAESSLTLNRLAGKQMIQVVKWAKVLP 788
Qy 728 GFRLNHYDDQMAVIOYSWMLGMVFMAGWRSFTNVNSRMLYFAPDLVFNEMRHKSMYSQ 787
Db 789 GFKNLPLEDQITLIOYSWMLSSSFALSWSRYSKHTNSQFLYFAPDLVFNEMRHKSMYEL 848

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QY	788	CVMRHLSDQFGLWLTPTQFELCMKALLFLSPVVDGLKNQKFFDELNMNLIKELDRITA	847
Db	849	COGMHOISLQFVRLQTLTFEYITLVLLSTIPKDLKSQAFAFEMRTNYIKELRKWMT	908
QY	848	CKRKNPTSCSRRYVLTKLDSVQPTARELHQFTTOLLKSKHMSVSDFFPMMAEISVQV	907
Db	909	KCPNNSQSWORYQYITKLKLDSDHDLVSDLEFCFYTFRESHALKVFEPPAMLVEISDQL	968
QY	908	PKILSGVKRPIYFH	921
Db	969	PKVESGNAPLXYFH	982
RESULT 15			
QRTG			
glucocorticoid receptor - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999			
C:Accession: A24194; S02475; A27284; S33888; S33891			
R:Miesfeld, R.; Rusconi, S.; Godowski, P.J.; Maler, B.A.; Okret, S.; Wikstrom, A.C.; Gus			
Cell 46, 389-399, 1986			
A:Title: Genetic complementation of a glucocorticoid receptor deficiency by expression o			
A:Reference number: A24194; MUID:86272086			
A:Accession: A24194			
A:Molecule type: mRNA			
A:Residues: 1-795 <MJE>			
A:Cross-references: GB:M14053; NID:g204271; PIDN:AAA41203.1; PID:g204272			
R:Severne, J.; Wieland, S.; Schaffner, W.; Rusconi, S.			
EMBO J. 7, 2503-2508, 1988			
A:Title: Metal binding 'finger' structures in the glucocorticoid receptor defined by sit			
A:Reference number: S02475; MUID:89052664			
A:Accession: S02475			
A:Status: not compared with conceptual translation			
A:Molecule type: mRNA			
R:Residues: 440-539 <SEV>			
R:Chang, C.; Kokontis, J.; Chang, C.T.; Liao, S.			
Nucleic Acids Res. 15, 9603, 1987			
A:Title: Cloning and sequence analysis of the rat ventral prostate glucocorticoid recept			
A:Reference number: A27284; MUID:88067783			
A:Accession: A27284			
A:Molecule type: mRNA			
A:Residues: 1-97, 'D', '99-225, 'G', 227-259, 'D', 261-344, 'T', 346-515 <CHA>			
A:Cross-references: GB:Y00489; NID:g56324; PIDN:CAA68545.1; PID:g56325			
R:Gearing, K.L.; Gustafsson, J.A.; Okret, S.			
Nucleic Acids Res. 21, 2014, 1993			
A:Title: Heterogeneity in the polyglutamine tract of the glucocorticoid receptor from di			
A:Reference number: S33888; MUID:93261843			
A:Accession: S33888			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 68-97, 'D', 99-104 <GEA>			
A:Cross-references: EMBL:X69666			
A:Accession: S33891			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 68-92, 97, 'D', 99-104 <GE2>			
A:Cross-references: EMBL:X69669			
C:Comment: This sequence contains five potential translation initiators: 1-Met, 28-Met,			
d is initiated from 1-Met.			
C:Superfamily: glucocorticoid receptor; erbA transforming protein homology			
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi			
F:75-96/Region: glutamine-rich			
F:138-692/Domain: erbA transforming protein homology <ERBA>			
F:440-460/Region: zinc finger CCCC motif			

Search completed: January 3, 2002, 23:07:40
Job time: 836 sec

Query Match	21.7%	Score 1065;	DB 1;	Length 795;
Best Local Similarity	32.0%;	pred. No. 4.5e-49;		
Matches	314;	Conservative 110;	Mismatches 268;	Indels 288;
				Gaps 35;

QY 20 RGAFQNLFSVR---EVIQNPGPRHPPEAASAPPGASLLL-----QQQQQQQQQQQ 68